AMENDMENTS TO THE SPECIFICATION

Please delete the paper copy of sequence listing previously submitted in the Preliminary Amendment dated September 8, 2005 and replace with the sequence listing submitted on compact disc enclosed herewith.

In the specification at page 1, after the section entitled "RELATED APPLICATIONS" inserted in the Preliminary Amendment, please insert the following new paragraph:

SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: two copies of the Sequence Listing (COPY 1 and COPY 2) and a computer readable form copy of the Sequence Listing (CRF COPY), all on compact disc , each containing: file name: Sequence listing - 12810-00137-US, date recorded: November 1, 2007, size: 166 KB.

In the specification at page 1, line 3, please replace the heading "Description" with the following heading:

BACKGROUND OF THE INVENTION

In the specification at page 4, line 22, please insert the following heading:

BRIEF SUMMARY OF THE INVENTION

In the specification at page 4, line 37, please insert the following paragraphs:

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1a-c: Alignment of protein sequences of different BI-1 proteins from plants. AtBI-1 (SEQ ID NO: 64): Arabidopsis; BnBI-1 (SEQ ID NO: 65): Brassica napus (oilseed rape); GmBI2 (SEQ ID NO: 12): Glycine max (soybean; variant 1); GmBI3 (SEQ ID NO: 66): Glycine max (soybean; variant 2); HVBI-1 (SEQ ID NO: 2): Hordeum vulgare (barley); NtBI-1 (SEQ ID NO: 67): Nicotiana tabacum (tobacco); OsBI-1 (SEQ ID NO: 68): Oryza sativa (rice); TaBI11 (SEQ ID NO: 20): Triticum aestivum (wheat, variant 1); TaBI18 (SEQ ID NO: 26): Triticum aestivum (wheat, variant 2); TaBI5 new (SEQ ID NO: 16): Triticum aestivum (wheat, variant 3); ZmBI14 (SEQ ID NO: 22): Zea mays (maize; variant 1); ZmBI16 (SEQ ID NO: 24): Zea mays (maize; variant 2); ZmBI33 (SEQ ID NO: 28): Zea mays (maize; variant 3); ZmBI8 (SEQ ID

NO: 18): Zea mays (maize; variant 4); Consensus: consensus sequence derived from the alignment.

Fig. 2: Vector map for the vector pUbiBI-1 (Ubi: ubiquitin promoter; BI-1 nucleic acid sequence coding for barley BI1 protein; ter: transcription terminator). Also shown are the localizations of the cleavage sites for different restriction enzymes.

Fig. 3: Vector map for the vector pLO114UbiBI-1 (Ubi: ubiquitin promoter; BI-1 nucleic acid sequence coding for barley BI1 protein; ter: transcription terminator). Also shown are the localizations of the cleavage sites for different restriction enzymes.

Fig. 4: Vector map for the vector pOxoBI-1 (Oxo: TaGermin 9f-2.8 promoter; BI-1 nucleic acid sequence coding for barley BI1 protein; ter: transcription terminator). Also shown are the localizations of the cleavage sites for different restriction enzymes.

Fig. 5: Vector map for the vector pLO114OxoBI-1 (Oxo: TaGermin 9f-2.8 promoter; BI-1 nucleic acid sequence coding for barley BI1 protein; ter: transcription terminator). Also shown are the localizations of the cleavage sites for different restriction enzymes.

Fig. 6: Alignment of the protein sequences of BI-1 proteins from barley *(Hordeum vulgare*, GenBank Acc. No.: CAC37797, SEQ ID NO: 2), rice *(Oryza sativa,* GenBank Acc. No.: Q9MBD8, SEQ ID NO: 8), *Arabidopsis thaliana* (GenBank Acc. No.: Q9LD45, SEQ ID NO: 4) and humans *(Homo sapiens,* GenBank Acc. No.: AAB87479, SEQ ID NO: 69). Amino acids shown against the black background are identical in all species. Amino acids shown against the gray background are identical in plants only. Bars indicate the predicted seven transmembrane domains in HvBI-1.

Fig. 7: BI-1 expression in resistant and susceptible barley lines (cDNA gel blot analysis): cDNAs were synthesized by means of RT-PCR, starting from total RNA. Total RNA was obtained from the susceptible barley line Pallas, the resistant barley line BC*PM1a12* and the resistant barley line BC*Pm1o5* at times 0 (i.e. immediately prior to inoculation) and in each case 1, 4 and 7 days after inoculation with *Bgh* and, in parallel, from uninfected control plants (Ø). The RT-PCR for *BI-1* was carried out using 20 cycles (see hereinbelow). The amount of RNA employed (0.5 µg) was additionally checked in gels by means of rRNA staining with ethidium bromide. A repetition of the experiments gave comparable results.

Fig. 8: *BI-1* is expressed in mesophyll tissue (cDNA gel blot analysis). RT-PCR was carried out starting from RNA isolated from Pallas (P) and BC*PMla12* (P10) (24 h after inoculation with *Bg*hA6). To extract the total RNA, abaxial epidermal strips (E, inoculated positions of the leaves) were separated from the mesophyll and the adaxial epidermis (M). *Ubiquitin 1 (Ubi)* was used as label for tissue-unspecific gene expression. RT-PCR was carried out using 30 cycles.

Fig. 9: *BI-1* expression is repressed during chemical resistance induction.

(A) Chemical induced resistance in the barley line Pallas gg. Blumeria graminis (DC) Speer f.sp. hordei (Bgh). Barley primary leaves were treated with 2,6-dichloroisonicotinic acid (DCINA) and showed fewer mildew pustules than corresponding untreated control plants.

(B) RNA and cDNA Blots. RNA (10 µg) was analyzed 0, 1, 2 and 3 days after soil treatment (soil drench treatment; dpt) with DCINA and with the control (carrier substance) and additionally 1 and 4 days post-inoculation (dpi, corresponds to 4 and 7 dpt, respectively). RT-PCR *(Ubi, BI-*1) was carried out using 20 cycles. Repetition resulted in comparable results (see Example 2).

BCI-4 was employed as the control. BCI-4 is a DCINA-induced gene (Besser et al. (2000) Mol Plant Pahol. 1(5): 277-286) and a member of the Barley Chemically (=BTH) induced gene family.

Fig. 10: Overexpression of *BI-1* induced supersusceptibility.

(A) Mean penetration efficiency of *Bgh* in 6 independent experiments with *Bgh* on barley line Ingrid. The PE of *Bgh* was significantly increased ($p<0.01$, Student's t-test) in cells which were transformed with *pBI-1* (by bombardment) in comparison with cells which were bombarded with the blank vector control (*pGY1*).

(B) The penetration efficiency of *Bgh* on cells which had been bombarded with an antisense *BI-1* construct (*pasBI-1*) was not significantly reduced ($p>0.05$) in comparison with cells which had been bombarded with the blank vector control (*pGY1*).

The columns show in each case the mean value of the individual experiments. The bars represent the standard error.

Fig. 11: Overexpression of *BI-1* induced breaking of the *mlo5*-mediated penetration resistance.

The penetration efficiency of *Bgh* was assessed in 3 to 4 independent experiments using *Bgh* on the barley lines Ingrid-*mlo5* and pallas-*mlo5*. The PE caused by *Bgh* was significantly increased ($p<0.05$) in cells which had been transformed with *pBI-1* (bombarded) in comparison with cells which had been bombarded with the blank vector control (*pGY1*). The columns show in each case the mean value of three independent experiments. The bars represent the standard error.

Fig. 12: The expression of *BI-1* is induced by toxic culture filtrates from *Bipolaris sorokiniana*. Northern blots (10 µg total RNA) with RNA from Ingrid (I) and BCIngrid-*mlo5* (I22). RNA was isolated 0, 24, 48 and 72 hours after injection of the toxic culture filtrates of *Bipolaris sorokiniana* (T) or water (W). BI-1 mRNAs were detected on nylon membranes following stringent washing. *BI-1*: detection of BAX Inhibitor 1 mRNA; *Ubi:* detection of *Ubiquitin 1; Asprot:* detection of the aspartate protease mRNA; hat: hours after treatment ("h after treatment").

Fig. 13: BI-1 overexpression breaks non-host resistance of barley (cv. Manchuria) to *Blumeria graminis* f.sp. *tritici.* The penetration rates were analyzed in three independent experiments.

DETAILED DESCRIPTION OF THE INVENTION

In the specification at page 38, lines 33-34, please delete the paragraph which starts with "Further translations can be found" and ends with "pilz.htm."

In the specification at pages 77-80, please delete the section under the heading entitled "Figures."